

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10|534486  
Source: PCT  
Date Processed by STIC: 5/19/15

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## RAW SEQUENCE LISTING

DATE: 05/19/2005

PATENT APPLICATION: US/10/534,486

TIME: 10:29:22

Input Set : A:\3121us0p.seq.txt

Output Set: N:\CRF4\05182005\J534486.raw

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3 <110> APPLICANT: MATSUO, Takanori
4     TSUGE, Hiroko
5     HAZAMA, Masatoshi
7 <120> TITLE OF INVENTION: Screening Method
9 <130> FILE REFERENCE: 3121US0P
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/534,486
C--> 11 <141> CURRENT FILING DATE: 2005-05-11
11 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/014339
12 <151> PRIOR FILING DATE: 2003-11-12
14 <150> PRIOR APPLICATION NUMBER: JP 2002-329778
15 <151> PRIOR FILING DATE: 2002-11-13
17 <160> NUMBER OF SEQ ID NOS: 3
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 432
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(432)
29 <223> OTHER INFORMATION:
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32 atg aaa tcc caa tgg tgt aga cca gtg gcg atg gat cta gga gtt tac      48
33 Met Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val Tyr
34 1                               5                               10                               15
36 caa ctg aga cat ttt tca att tct ttc ttg tca tcc ttg ctg ggg act      96
37 Gln Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly Thr
38 20                               25                               30
40 gaa aac gct tct gtg aga ctt gat aat agc tcc tct ggt gca agt gtg      144
41 Glu Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser Val
42 35                               40                               45
44 gta gct att gac aac aaa atc gag caa gct atg gat cta gtg aaa agc      192
45 Val Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Ser
46 50                               55                               60
48 cat ttg atg tat gcg gtc aga gaa gaa gtg gag gtc ctc aaa gag caa      240
49 His Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln
50 65                               70                               75                               80
52 atc aaa gaa cta ata gag aaa aat tcc cag ctg gag cag gag aac aat      288
53 Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn Asn
54 85                               90                               95
56 ctg ctg aag aca ctg gcc agt cct gag cag ctt gcc cag ttt cag gcc      336
57 Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln Ala
58 100                               105                               110

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60 cag ctg cag act ggc tcc ccc cct gcc acc acc cag cca cag ggc acc      384
61 Gln Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly Thr
62      115      120      125
64 aca cag ccc ccc gcc cag cca gca tcg cag ggc tca gga cca acc gca      432
65 Thr Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr Ala
66      130      135      140
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70 <211> LENGTH: 144
71 <212> TYPE: PRT
72 <213> ORGANISM: Homo sapiens
74 <400> SEQUENCE: 2
76 Met Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val Tyr
77 1      5      10      15
80 Gln Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly Thr
81      20      25      30
84 Glu Asn Ala Ser Val Arg Leu Asp Asn Ser Ser Ser Gly Ala Ser Val
85      35      40      45
88 Val Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Ser
89      50      55      60
92 His Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln
93 65      70      75      80
96 Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu Gln Glu Asn Asn
97      85      90      95
100 Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Ala Gln Phe Gln Ala
101      100      105      110
104 Gln Leu Gln Thr Gly Ser Pro Pro Ala Thr Thr Gln Pro Gln Gly Thr
105      115      120      125
108 Thr Gln Pro Pro Ala Gln Pro Ala Ser Gln Gly Ser Gly Pro Thr Ala
109      130      135      140
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 342
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence
117 <220> FEATURE:
118 <223> OTHER INFORMATION: DNA used as sense probe for in situ hybridization analysis
in
119      Example 4.
121 <400> SEQUENCE: 3
122 gcctgctatg ccccaacaga actggctgct gctgtctgaa ctgaacagac cgaagagatg      60
124 tgctagttag aagccgcctc cagtcaccca ttctattgct gtctgcgaaa gagacgtgag      120
126 actcacacat gctgttctcg ctttctcccc agtattaagc actcatatgc ttttggttg      180
128 aagaaatata ctagttagt gaattaaagg ttaaacagag agtgagcatg gatgtaccct      240
130 gtgcaacgtg gcagatgtct gaggaatggt ttgattgacg ctgaggagga gctctgtgcc      300
132 ttttcaaccc tccccagccg cccactctac tccaagctc tg      342

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**VERIFICATION SUMMARY**

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:31 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:29